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## RAW SEQUENCE LISTING

DATE: 12/18/2002

PATENT APPLICATION: US/09/549,096C

TIME: 12:21:06

Input Set : A:\LIAI-0276397.txt

Output Set: N:\CRF4\12182002\I549096C.raw

ENTERED

```

4 <110> APPLICANT: La Jolla Institute for Allergy and Immunology
5     Ware, Carl F.
7 <120> TITLE OF INVENTION: LIGAND FOR HERPES SIMPLEX VIRUS ENTRY
8     MEDIATOR AND METHODS OF USE
10 <130> FILE REFERENCE: 051501-0276397
12 <140> CURRENT APPLICATION NUMBER: 09/549,096C
13 <141> CURRENT FILING DATE: 2000-04-12
15 <150> PRIOR APPLICATION NUMBER: 08/898,234
16 <151> PRIOR FILING DATE: 1997-07-30
18 <150> PRIOR APPLICATION NUMBER: 60/051,964
19 <151> PRIOR FILING DATE: 1997-07-07
21 <160> NUMBER OF SEQ ID NOS: 16
23 <170> SOFTWARE: PatentIn Ver. 2.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 29
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Description of Artificial Sequence:
32     Forward primer sequence
34 <400> SEQUENCE: 1
36 cggagatctg agttcatcct gctagctgg      29
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 31
41 <212> TYPE: DNA
42 <213> ORGANISM: Artificial Sequence
44 <220> FEATURE:
45 <223> OTHER INFORMATION: Description of Artificial Sequence:
46     Backward primer sequence
48 <400> SEQUENCE: 2
50 ataggatccc ttggtctggt gctgacattc c    31
53 <210> SEQ ID NO: 3
54 <211> LENGTH: 29
55 <212> TYPE: DNA
56 <213> ORGANISM: Artificial Sequence
58 <220> FEATURE:
59 <223> OTHER INFORMATION: Description of Artificial Sequence:
60     Forward primer sequence
62 <400> SEQUENCE: 3
64 gacgtcagat cttccacacct ttcctccta      29
67 <210> SEQ ID NO: 4
68 <211> LENGTH: 29
69 <212> TYPE: DNA

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70 <213> ORGANISM: Artificial Sequence
72 <220> FEATURE:
73 <223> OTHER INFORMATION: Description of Artificial Sequence:
74     Backward primer sequence
76 <400> SEQUENCE: 4
78 gaacagagat ctcattgctc ctggctctg      29
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83 <211> LENGTH: 1169
84 <212> TYPE: DNA
85 <213> ORGANISM: Homo sapiens
87 <220> FEATURE:
88 <221> NAME/KEY: CDS
89 <222> LOCATION: (49)..(771)
91 <400> SEQUENCE: 5
92 gaggttgaag gaccagggcg tgtcagccct gctccagaga ccttgggc atg gag gag      57
93                                     Met Glu Glu
94                                     1
96 agt gtc gta cgg ccc tca gtg ttt gtg gtg gat gga cag acc gac atc      105
97 Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln Thr Asp Ile
98     5             10             15
100 cca ttc acg agg ctg gga cga agc cac cgg aga cag tcg tgc agt gtg      153
101 Pro Phe Thr Arg Leu Gly Arg Ser His Arg Arg Gln Ser Cys Ser Val
102 20             25             30             35
104 gcc cgg gtg ggt ctg ggt ctc ttg ctg ttg ctg atg ggg gct ggg ctg      201
105 Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Leu Met Gly Ala Gly Leu
106             40             45             50
108 gcc gtc caa ggc tgg ttc ctc ctg cag ctg cac tgg cgt cta gga gag      249
109 Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg Leu Gly Glu
110             55             60             65
112 atg gtc acc cgc ctg cct gac gga cct gca ggc tcc tgg gag cag ctg      297
113 Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp Glu Gln Leu
114             70             75             80
116 ata caa gag cga agg tct cac gag gtc aac cca gca gcg cat ctc aca      345
117 Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala His Leu Thr
118             85             90             95
120 ggg gcc aac tcc agc ttg acc ggc agc ggg ggg ccg ctg tta tgg gag      393
121 Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu Leu Trp Glu
122 100             105             110             115
124 act cag ctg ggc ctg gcc tcc ctg agg ggc ctc agc tac cac gat ggg      441
125 Thr Gln Leu Gly Leu Ala Ser Leu Arg Gly Leu Ser Tyr His Asp Gly
126             120             125             130
128 gcc ctt gtg gtc acc aaa gct ggc tac tac tac atc tac tcc aag gtg      489
129 Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr Ser Lys Val
130             135             140             145
132 cag ctg ggc ggt gtg ggc tgc ccg ctg ggc ctg gcc agc acc atc acc      537
133 Gln Leu Gly Gly Val Gly Cys Pro Leu Gly Leu Ala Ser Thr Ile Thr
134             150             155             160
136 cac ggc ctc tac aag cgc aca ccc cgc tac ccc gag gag ctg gag ctg      585
137 His Gly Leu Tyr Lys Arg Thr Pro Arg Tyr Pro Glu Glu Leu Glu Leu

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138      165      170      175
140 ttg gtc agc cag cag tca ccc tgc gga cgg gcc acc agc agc tcc cgg 633
141 Leu Val Ser Gln Gln Ser Pro Cys Gly Arg Ala Thr Ser Ser Ser Arg
142 180      185      190      195
144 gtc tgg tgg gac agc agc ttc ctg ggt ggt gtg gta cac ctg gag gct 681
145 Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His Leu Glu Ala
146      200      205      210
148 ggg gag gag gtg gtc gtc cgt gtg ctg gat gaa cgc ctg gtt cga ctg 729
149 Gly Glu Glu Val Val Val Arg Val Leu Asp Glu Arg Leu Val Arg Leu
150      215      220      225
152 cgt gat ggt acc cgg tct tac ttc ggg gct ttc atg gtg tga 771
153 Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val
154      230      235      240
156 aggaaggagc gtggtgcatt ggacatgggt ctgacacgtg gagaactcag aggggtgcctc 831
158 aggggaaaga aaactcacga agcagaggct gggcgtgggt gctctcgct gtaatcccag 891
160 cactttggga ggccaaggca ggcggatcac ctgagggtcag gagttcgaga ccagcctggc 951
162 taacatggca aaaccccatc tctactaaaa atacaaaaat tagccggacg tgggtggtgcc 1011
164 tgccgtgaat ccagctactc aggaggctga ggcaggataa ttttgcttaa acccgggagg 1071
166 cggagggttg agtgagccga gatcacacca ctgcactcca acctgggaaa cgcagtgaga 1131
168 ctgtgcctca aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1169
172 <210> SEQ ID NO: 6
173 <211> LENGTH: 240
174 <212> TYPE: PRT
175 <213> ORGANISM: Homo sapien
177 <400> SEQUENCE: 6
179 Met Glu Glu Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln
180 1      5      10      15
183 Thr Asp Ile Pro Phe Thr Arg Leu Gly Arg Ser His Arg Arg Gln Ser
184      20      25      30
187 Cys Ser Val Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Leu Met Gly
188      35      40      45
191 Ala Gly Leu Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg
192      50      55      60
195 Leu Gly Glu Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp
196 65      70      75      80
199 Glu Gln Leu Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala
200      85      90      95
203 His Leu Thr Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu
204      100      105      110
207 Leu Trp Glu Thr Gln Leu Gly Leu Ala Phe Leu Arg Gly Leu Ser Tyr
208      115      120      125
211 His Asp Gly Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr
212      130      135      140
215 Ser Lys Val Gln Leu Gly Gly Val Gly Cys Pro Leu Gly Leu Ala Ser
216 145      150      155      160
219 Thr Ile Thr His Gly Leu Tyr Lys Arg Thr Pro Arg Tyr Pro Glu Glu
220      165      170      175
223 Leu Glu Leu Leu Val Ser Gln Gln Ser Pro Cys Gly Arg Ala Thr Ser
224      180      185      190

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304 <213> ORGANISM: Artificial Sequence
306 <220> FEATURE:
307 <223> OTHER INFORMATION: Description of Artificial Sequence:
308     Forward primer sequence
310 <220> FEATURE:
311 <221> NAME/KEY: misc_feature
312 <222> LOCATION: (10)...(10)
313 <223> OTHER INFORMATION: N=Inosine
315 <400> SEQUENCE: 11
W--> 317 gagctggccn tgctgagggg cct      23
320 <210> SEQ ID NO: 12
321 <211> LENGTH: 20
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial Sequence
325 <220> FEATURE:
326 <223> OTHER INFORMATION: Description of Artificial Sequence:
327     Backward primer sequence
329 <400> SEQUENCE: 12
331 cagctgagtc tcccataaca      20
334 <210> SEQ ID NO: 13
335 <211> LENGTH: 22
336 <212> TYPE: DNA
337 <213> ORGANISM: Artificial Sequence
339 <220> FEATURE:
340 <223> OTHER INFORMATION: Description of Artificial Sequence:
341     Forward primer sequence
343 <220> FEATURE:
344 <221> NAME/KEY: misc_feature
345 <222> LOCATION: (7)...(7)
346 <223> OTHER INFORMATION: N=Inosine
349 <400> SEQUENCE: 13
W--> 351 caggccntcc tgaggggcct ca      22
354 <210> SEQ ID NO: 14
355 <211> LENGTH: 21
356 <212> TYPE: DNA
357 <213> ORGANISM: Artificial Sequence
359 <220> FEATURE:
360 <223> OTHER INFORMATION: Description of Artificial Sequence:
361     Backward primer sequence
363 <400> SEQUENCE: 14
365 gcccagctga gtctcccata a      21
368 <210> SEQ ID NO: 15
369 <211> LENGTH: 20
370 <212> TYPE: DNA
371 <213> ORGANISM: Artificial Sequence
373 <220> FEATURE:
374 <223> OTHER INFORMATION: Description of Artificial Sequence:
375     Forward primer sequence
377 <400> SEQUENCE: 15

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/549,096C

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Input Set : A:\LIAI-0276397.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 17  
Seq#:11; N Pos. 10  
Seq#:13; N Pos. 7

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5,10,12,15,21,23,25,26,27,28,30,39  
Seq#:2; Line(s) 40,41,42,44,53  
Seq#:3; Line(s) 54,55,56,58,67  
Seq#:4; Line(s) 69,70,72  
Seq#:6; Line(s) 240  
Seq#:7; Line(s) 242,243,245,250  
Seq#:8; Line(s) 255,256,257,259,264

US 095490960LP1



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Legal Date: 20-08-2003

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1	EXIN	2

Total number of pages: 2

Remarks:

Order of re-scan issued on .....